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Novel poly(ADP-ribose) polymerase genes

The present invention relates to novel poly(ADP-ribose) polymerase (PARP) genes and to the proteins derived therefrom; antibodies with specificity for the novel proteins; pharmaceutical and gene therapy compositions which comprise products according to the invention; methods for the analytical determination of the proteins and nucleic acids according to the invention; methods for identifying effectors or binding partners of the proteins according to the invention; methods for determining the activity of such effectors and use thereof for the diagnosis or therapy of pathological states.

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In 1966, Chambon and co-workers discovered a 116 kD enzyme which was characterized in detail in subsequent years and is now called PARP (EC 2.4.2.30) (poly(adenosine-5'-diphosphoribose) polymerase), PARS (poly(adenosine-5'-diphosphoribose) synthase) or ADPRT (adenosine-5'-diphosphoribose transferase). In the plant kingdom (*Arabidopsis thaliana*) a 72kD (637 amino acids) PARP was found in 1995 (Lepiniec L. et al., FEBS Lett 1995; 364(2): 103-8). It was not clear whether this shorter form of PARP is a plant-specific individuality or an artefact ("splice" variant or the like). The 116 kD PARP enzyme has to date been unique in animals and in man in its activity, which is described below. It is referred to as PARP1 below to avoid ambiguity.

The primary physiological function of PARP 1 appears to be its involvement in a complex repair mechanism which cells have developed to repair DNA strand breaks. The primary cellular response to a DNA strand break appears moreover to consist of PARP1-catalyzed synthesis of poly(ADP-ribose) from NAD^+ (cf. De Murcia, G. et al. (1994) TIBS, 19, 172).

PARP 1 has a modular molecular structure. Three main functional elements have been identified to date: an N-terminal 46 kD DNA binding domain; a central 22 kD automodification domain to which poly(ADP-ribose) becomes attached, with the PARP 1 enzyme activity decreasing with increasing elongation; and a C-terminal 54 kD NAD^+ binding domain. A leucine zipper region has been found within the automodification domain, indicating possible protein-protein interactions, only in the PARP from Drosophila. All PARPs known to date are presumably active as homodimers.

The high degree of organization of the molecule is reflected in the strong conservation of the amino acid sequence. Thus, 62% conservation of the amino acid sequence has been found for PARP 1

from humans, mice, cattle and chickens. There are greater structural differences from the PARP from Drosophila. The individual domains themselves in turn have clusters of increased conservation. Thus, the DNA binding region contains two so-called zinc fingers as subdomains (comprising motifs of the type $CX_2CX_{28/30}HX_2C$), which are involved in the Zn^{2+}-dependent recognition of DNA single strand breaks or single-stranded DNA overhangs (e.g. at the chromosome ends, the telomeres). The C-terminal catalytic domain comprises a block of about 50 amino acids (residues 859-908), which is about 100% conserved among vertebrates (PARP "signature"). This block binds the natural substrate NAD^+ and thus governs the synthesis of poly(ADP-ribose) (cf. de Murcia, loc.cit.). The GX_3GKG motif in particular is characteristic of PARPs in this block.

The beneficial function described above contrasts with a pathological one in numerous diseases (stroke, myocardial infarct, sepsis etc.). PARP is involved in cell death resulting from ischemia of the brain (Choi, D.W., (1997) Nature Medicine, 3, 10, 1073), of the myocardium (Zingarelli, B., et al (1997), Cardiovascular Research, 36, 205) and of the eye (Lam, T.T. (1997), Res. Comm. in Molecular Pathology and Pharmacology, 95, 3, 241). PARP activation induced by inflammatory mediators has also been observed in septic shock (Szabo, C., et al. (1997), Journal of Clinical Investigation, 100, 3, 723). In these cases, activation of PARP is accompanied by extensive consumption of NAD^+. Since four moles of ATP are consumed for the biosynthesis of one mole of NAD^+, the cellular energy supply decreases drasticallly. The consequence is cell death.

PARP1 inhibitors described in the abovementioned specialist literature are nicotinamide and 3-aminobenzamide. 3,4-Dihydro-5-[4-(1-piperidinyl)butoxy]-1(2H)-isoquinolone is disclosed by Takahashi, K., et al (1997), Journal of Cerebral Blood Flow and Metabolism 17, 1137. Further inhibitors are described, for example, in Banasik, M., et al. (1992) J. Biol. Chem., 267, 3, 1569 and Griffin, R.J., et al. (1995), Anti-Cancer Drug Design, 10, 507.

High molecular weight binding partners described for human PARP1 include the base excision repair (BER) protein XRCC1 (X-ray repair cross-complementing 1) which binds via a zinc finger motif and a BRCT (BRCA1 C-terminus) module (amino acids 372-524) (Masson, M., et al., (1998) Molecular and Cellular Biology, 18,6, 3563).

It is an object of the present invention, because of the diverse physiological and pathological functions of PARP, to provide novel PARP homologs. The reason for this is that the provision of homologous PARPs would be particularly important for developing novel targets for drugs, and novel drugs, in order to improve diagnosis and/or therapy of pathological states in which PARP, PARP homologs or substances derived therefrom are involved.

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We have found that this object is achieved by providing PARP homologs, preferably derived from human and non-human mammals, having an amino acid sequence which has

a) a functional NAD^+ binding domain, i.e. a PARP "signature" sequence having the characteristic GX_3GKG motif;
and
b) especially in the N-terminal sequence region, i.e. in the region of the first 200, such as, for example, in the region of the first 100, N-terminal amino acids, no PARP zinc finger sequence motifs of the general formula

$$CX_2CX_mHX_2C$$

in which
m is an integral value from 28 or 30, and the X radicals are, independently of one another, any amino acid;

and the functional equivalents thereof.

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Since the PARP molecules according to the invention represent in particular functional homologs, they naturally also have a poly(ADP-ribose)-synthesizing activity. The NAD binding domain essentially corresponds to this activity and is localized to the C terminus.

Thus an essential characteristic of the PARPs according to the invention is the presence of a functional NAD^+ binding domain (PARP signature) which is located in the C-terminal region of the amino acid sequence (i.e. approximately in the region of the last 400, such as, for example, the last 350 or 300, C-terminal amino acids), in combination with an N-terminal sequence having no zinc finger motifs. Since the zinc finger motifs in known PARPs presumably contribute to recognition of the DNA breakages, it is to be assumed that the proteins according to the invention do not interact with DNA or do so in another way. It has been demonstrated by appropriate biochemical tests that the PARP2 according to the invention can be activated by 'activated DNA' (i.e. DNA after limited DNaseI digestion). It can be concluded from this further that the PARP2 according to the invention has DNA binding properties. However, the mechanism of the DNA binding and enzyme activation differs between the PARPs according to the invention and PARP1. Its DNA binding and enzyme activation is, as

mentioned, mediated by a characteristic zinc finger motif. No such motifs are present in the PARPs according to the invention. Presumably these properties are mediated by positively charged amino acids in the N-terminal region of the PARPs according to the invention. Since the 'activated DNA' (i.e. for example DNA after limited treatment with DNaseI) has a large number of defects (single strand breaks, single strand gaps, single-stranded overhangs, double strand breaks etc.), it is possible that although PARP1 and the PARPs according to the invention are activated by the same 'activated DNA', it is by a different subpopulation of defects (e.g. single strand gaps instead of single strand breaks).

The functional NAD^+ binding domain (i.e. catalytic domain) binds the substrate for poly-(ADP-ribose) synthesis. Consistent with known PARPs, the sequence motif $GX^1X^2X^3GKG$, in which G is glycine, K is lysine, and X^1, X^2 and X^3 are, independently of one another, any amino acid, is present in particular. However, as shown, surprisingly, by comparison of the amino acid sequences of the NAD^+ binding domains of PARP molecules according to the invention with previously disclosed human PARP1, the sequences according to the invention differ markedly from the known sequence for the NAD^+ binding domain.

A group of PARP molecules which is preferred according to the invention preferably has the following general sequence motif in the catalytic domain in common:

$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11), in particular
$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12),
preferably
$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$
(SEQ ID NO:13)

in which (S/T) describes the alternative occupation of this sequence position by S or T, (I/V) describes the alternative occupation of this sequence position by I or V, and n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid. The last motif is also referred to as the "PARP signature" motif.

The automodification domain is preferably likewise present in the PARPs according to the invention. It can be located, for example, in the region from about 100 to 200 amino acids in front of the N-terminal end of the NAD^+ binding domain.

PARP homologs according to the invention may additionally comprise, N-terminally of the NAD^+ binding domain (i.e. about 30 to about 80 amino acids closer to the N terminus), a leucine zipper-like sequence motif of the general formula

(L/V)X_6LX_6LX_6L (SEQ ID NO:14)

in which

(L/V) represents the alternative occupation of this sequence position by L or V, and the X radicals are, independently of one another, any amino acid. The leucine zipper motifs observed according to the invention differ distinctly in position from those described for PARP from Drosophila. Leucine zippers may lead to homodimers (two PARP molecules) or heterodimers (one PARP molecule with a binding partner differing therefrom).

The PARP homologs according to the invention preferably additionally comprise, N-terminally of the abovementioned leucine zipper-like sequence motifs, i.e. about 10 to 250 amino acid residues closer to the N terminus, at least another one of the following part-sequence motifs:

LX_9NX_2YX_2QLLX(D/E)X_bWGRVG, (motif 1; SEQ ID NO:15)
AX_3FXKKX_4KTXNXWX$_5$FX_3PXK, (motif 2; SEQ ID NO:16)
QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L, (motif 3; SEQ ID NO:17)
FYTXIPHXFGX_3PP, (motif 4; SEQ ID NO:18)
and
KX_3LX_2LXDIEXAX_2L (motif 5; SEQ ID NO:19),

in which (D/E) describes the alternative occupation of this sequence position by D or E, (I/L) describes the alternative occupation of this sequence position by I or L, b is the integral value 10 or 11, and the X radicals are, independently of one another, any amino acid. It is most preferred for these motifs 1 to 5 all to be present in the stated sequence, with motif 1 being closest to the N terminus.

The abovementioned PARP signature motif is followed in the proteins according to the invention by at least another one of the following motifs:

GX_3LXEVALG (motif 6; SEQ ID NO:20)
GX_2SX_4GX_3PX_aLXGX_2V (motif 7; SEQ ID NO:21) and
E(Y/F)X_2YX_3QX_4YLL (motif 8; SEQ ID NO:22)

in which (Y/F) describes the alternative occupation of this sequence position by Y or F, a is equal to 7 to 9 and X is in each case any amino acid. It is most preferred for the three

C-terminal motifs all to be present and in the stated sequence, with motif 8 being closest to the C terminus.

A preferred PARP structure according to the invention may be described schematically as follows:

Motifs 1 to 5/PARP signature/motifs 6 to 8 or
motifs 1 to 5/leucine zipper/PARP signature/motifs 6 to 8

it being possible for further amino acid residues, such as, for example, up to 40, to be arranged between the individual motifs and for further amino acid residues, such as, for example, up to 80, to be arranged at the N terminus and/or at the C terminus.

PARP homologs which are particularly preferred according to the invention are the proteins human PARP2, human PARP3, mouse PARP3 and the functional equivalents thereof. The protein referred to as human PARP2 comprises 570 amino acids (cf. SEQ ID NO:2). The protein referred to as human PARP3 possibly exists in two forms. Type 1 comprises 533 amino acids (SEQ ID NO:4) and type 2 comprises 540 amino acids (SEQ ID NO:6). The forms may arise through different initiation of translation. The protein referred to as mouse PARP3 exists in two forms which differ from one another by a deletion of 5 amino acids (15 bp). Type 1 comprises 533 amino acids (SEQ ID NO: 8) and type 2 comprises 528 amino acids (SEQ ID NO:10). The PARP-homologs of the present invention differ in their sequences significantly over said PARP protein of Arabidopsis thaliana (see above). For example, PARP2 and PARP3 do not comprise the plant PARP specific peptide sequence AAVLDQWIPD, corresponding to amino acid residues 143 to 152 of the Arabidopsis protein.

The invention further relates to the binding partners for the PARP homologs according to the invention. These binding partners are preferably selected from

a) antibodies and fragments such as, for example, Fv, Fab, $F(ab')_2$, thereof
b) protein-like compounds which interact, for example via the above leucine zipper region or another sequence section, with PARP, and
c) low molecular weight effectors which modulate a biological PARP function such as, for example, the catalytic PARP activity, i.e. NAD^+-consuming ADP ribosylation, or the binding to an activator protein or to DNA.

The invention further relates to nucleic acids comprising

a) a nucleotide sequence coding for at least one PARP homolog according to the invention, or the complementary nucleotide sequence thereof;
b) a nucleotide sequence which hybridizes with a sequence as specified in a), preferably under stringent conditions; or
c) nucleotide sequences which are derived from the nucleotide sequences defined in a) and b) through the degeneracy of the genetic code.

Nucleic acids which are suitable according to the invention comprise in particular at least one of the partial sequences which code for the abovementioned amino acid sequence motifs.

Nucleic acids which are preferred according to the invention comprise nucleotide sequences as shown in SEQ ID NO: 1 and 3, and, in particular, partial sequences thereof which are characteristic of PARP homologs according to the invention, such as, for example, nucleotide sequences comprising

a) nucleotides +3 to +1715 shown in SEQ ID NO:1;
b) nucleotides +242 to +1843 shown in SEQ ID NO:3;
c) nucleotides +221 to +1843 shown in SEQ ID NO:5;
d) nucleotides +112 to +1710 shown in SEQ ID NO:7; or
e) nucleotides +1 to +1584 shown in SEQ ID NO:9

or partial sequences of a), b), c), d) and e) which code for the abovementioned characteristic amino acid sequence motifs of the PARP homologs according to the invention.

The invention further relates to expression cassettes which comprise at least one of the above-described nucleotide sequences according to the invention under the genetic control of regulatory nucleotide sequences. These can be used to prepare recombinant vectors according to the invention, such as, for example, viral vectors or plasmids, which comprise at least one expression cassette according to the invention.

Recombinant microorganisms according to the invention are transformed with at least one of the abovementioned vectors.

The invention also relates to transgenic mammals transfected with a vector according to the invention.

The invention further relates to an in vitro detection method, which can be carried out homogeneously or heterogeneously, for PARP inhibitors, which comprises

a) incubating an unsupported or supported poly-ADP-ribosylatable target with a reaction mixture comprising
   a1) a PARP homolog according to the invention;
   a2) a PARP activator; and
   a3) a PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected;
b) carrying out the polyADP ribosylation reaction; and
c) determining the polyADP ribosylation of the target qualitatively or quantitatively.

The detection method is preferably carried out by preincubating the PARP homolog with the PARP activator and the PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected, for example for about 1-30 minutes, before carrying out the poly-ADP ribosylation reaction.

After activation by DNA with single strand breaks (referred to as "activated DNA" according to the invention), PARP poly-ADP ribosylates a large number of nuclear proteins in the presence of NAD. These proteins include, on the one hand, PARP itself, but also histones etc.

The poly-ADP-ribosylatable target preferably used in the detection method is a histone protein in its native form or a poly-ADP-ribosylatable equivalent derived therefrom. A histone preparation supplied by Sigma (SIGMA, catalogue No. H-7755; histone type II-AS from calf thymus, Luck, J. M., et al., J. Biol. Chem., 233, 1407 (1958), Satake K., et al., J. Biol. Chem, 235, 2801 (1960)) was used by way of example. It is possible in principle to use all types of proteins or parts thereof amenable to poly-ADP-ribosylation by PARP. These are preferably nuclear proteins, e.g. histones, DNA polymerase, telomerase or PARP itself. Synthetic peptides derived from the corresponding proteins can also act as target.

In the ELISA according to the invention it is possible to use amounts of histones in the range from about 0.1 µg/well to about 100 µg/well, preferably about 1 µg/well to about 10 µg/well. The amounts of the PARP enzyme are in a range from about 0.2 pmol/well to about 2 nmol/well, preferably from about 2 pmol/well to about 200 pmol/well, the reaction mixture comprising in each case 100 µg/well. Reductions to smaller wells and correspondingly smaller reaction volumes are possible.

In the HTRF assay according to the invention, identical amounts of PARP are employed, and the amount of histone or modified histones is in the range from about 2 ng/well to about 25 µg/well,

preferably about 25 ng/well to about 2.5 µg/well, the reaction mixture comprising in each case 50 µl/well. Reductions to smaller wells and correspondingly smaller reaction volumes are possible.

The PARP activator used according to the invention is preferably activated DNA.

Various types of damaged DNA can function as activator. DNA damage can be produced by digestion with DNases or other DNA-modifying enzymes (e.g. restriction endonucleases), by irradiation or other physical methods or chemical treatment of the DNA. It is further possible to simulate the DNA damage situation in a targeted manner using synthetic oligonucleotides. In the assays indicated by way of example, activated DNA from calf thymus was employed (Sigma, product No. D4522; CAS: 91080-16-9, prepared by the method of Aposhian and Kornberg using calf thymus DNA (SIGMA D-1501) and deoxyribonuclease type I (D-4263). Aposhian H. V. and Kornberg A., J. Biol. Chem., 237, 519 (1962)). The activated DNA was used in a concentration range from 0.1 to 1000 µg/ml, preferably from 1 to 100 µg/ml, in the reaction step.

The polyADP ribosylation reaction is started in the method according to the invention by adding NAD^+. The NAD concentrations were in a range from about 0.1 µM to about 10 mM, preferably in a range from about 10 µM to about 1 mM.

In the variant of the above method which can be carried out heterogeneously, the polyADP ribosylation of the supported target is determined using anti-poly(ADP-ribose) antibodies. To do this, the reaction mixture is separated from the supported target, washed and incubated with the antibody. This antibody can itself be labeled. However, as an alternative for detecting bound anti-poly(ADP-ribose) antibody a labeled secondary antibody or a corresponding labeled antibody fragment may be applied. Suitable labels are, for example, radiolabeling, chromophore- or fluorophore-labeling, biotinylation, chemiluminescence labeling, labeling with paramagnetic material or, in particular, enzyme labels, e.g. with horseradish peroxidase. Appropriate detection techniques are generally known to the skilled worker.

In the variant of the above process which can be carried out homogeneously, the unsupported target is labeled with an acceptor fluorophore. The target preferably used in this case is biotinylated histone, the acceptor fluorophore being coupled via avidin or streptavidin to the biotin groups of the histone. Particularly suitable as acceptor fluorophore are phycobiliproteins (e.g. phycocyanins, phycoerythrins), e.g. R-phycocyanin (R-PC), allophyco-

cyanin (APC), R-phycoerythrin (R-PE), C-phycocyanin (C-PC), B-phycoerythrin (B-PE) or their combinations with one another or with fluorescent dyes such as Cy5, Cy7 or Texas Red (Tandem system) (Thammapalerd, N. et al., Southeast Asian Journal of Tropical Medicine & Public Health, 27(2): 297-303 (1996); Kronick, M. N. et al., Clinical Chemistry, 29(9), 1582-1586 (1986); Hicks, J. M., Human Pathology, 15(2), 112-116 (1984)). The dye XL665 used in the examples is a crosslinked allophycocyanin (Glazer, A. N., Rev. Microbiol., 36, 173-198 (1982); Kronick, M. N., J. Imm. Meth., 92, 1-13 (1986); MacColl, R. et al., Phycobiliproteins, CRC Press, Inc., Boca Raton, Florida (1987); MacColl, R. et al., Arch. Biochem. Biophys., 208(1), 42-48 (1981)).

It is additionally preferred in the homogeneous method to determine the polyADP ribosylation of the unsupported target using anti-poly(ADP-ribose) antibody which is labeled with a donor fluorophore which is able to transfer energy to the acceptor fluorophore when donor and acceptor are close in space owing to binding of the labeled antibody to the polyADP-ribosylated histone. A europium cryptate is preferably used as donor fluorophore for the anti-poly(ADP-ribose) antibody.

Besides the europium cryptate used, other compounds are also possible as potential donor molecules. This may entail, on the one hand, modification of the cryptate cage. Replacement of the europium by other rare earth metals such as terbium is also conceivable. It is crucial that the fluorescence has a long duration to guarantee the time delay (Lopez, E. et al., Clin. Chem. 39/2, 196-201 (1993); US Patent 5,534,622).

The detection methods described above are based on the principle that there is a correlation between the PARP activity and the amount of ADP-ribose polymers formed on the histones. The assay described herein makes it possible to quantify the ADP-ribose polymers using specific antibodies in the form of an ELISA and an HTRF (homogenous time-resolved fluorescence) assay. Specific embodiments of these two assays are described in detail in the following examples.

The developed HTRF (homogeneous time-resolved fluorescence) assay system measures the formation of poly(ADP-ribose) on histones using specific antibodies. In contrast to the ELISA, this assay is carried out in homogeneous phase without separation and washing steps. This makes a higher sample throughput and a smaller susceptibility to errors possible. HTRF is based on the fluorescence resonance energy transfer (FRET) between two fluorophores. In a FRET assay, an excited donor fluorophore can

transfer its energy to an acceptor fluorophore when the two are close to one another in space. In HTRF technology, the donor fluorophore is a europium cryptate [(Eu)K] and the acceptor is XL665, a stabilized allophycocyanin. The europium cryptate is based on studies by Jean Marie Lehn (Strasbourg) (Lopez, E. et al., Clin. Chem. 39/2, 196-201 (1993); US Patent 5,534,622).

In a homogeneous assay, all the components are also present during the measurement. Whereas this has advantages for carrying out the assay (rapidity, complexity), it is necessary to preclude interference by assay components (inherent fluorescence, quenching by dyes etc.). HTRF precludes such interference by time-delayed measurement at two wavelengths (665 nm, 620 nm). The HTRF has a very long decay time and time-delayed measurement is therefore possible. There is no longer any interference from short-lived background fluorescence (e.g. from assay components or inhibitors of the substance library). In addition, measurement is always carried out at two wavelengths in order to compensate for quench effects of colored substances. HTRF assays can be carried out, for example, in 96- or 384-well microtiter plate format and are evaluated using a discovery HTRF microplate analyzer (Canberra Packard).

Also provided according to the invention are the following in vitro screening methods for binding partners for PARP, in particular for a PARP homolog according to the invention.

A first variant is carried out by
a1) immobilizing at least one PARP homolog on a support;
b1) contacting the immobilized PARP homolog with an analyte in which at least one binding partner is suspected; and
c1) determining, where appropriate after an incubation period, analyte constituents bound to the immobilized PARP homolog.

A second variant entails
a2) immobilizing on a support an analyte which comprises at least one possible binding partner for the PARP homolog;
b2) contacting the immobilized analyte with at least one PARP homolog for which a binding partner is sought; and
c3) examining the immobilized analyte, where appropriate after an incubation period, for binding of the PARP homolog.

The invention also relates to a method for the qualitative or quantitative determination of a nucleic acid encoding a PARP homolog, which comprises

a) incubating a biological sample with a defined amount of an exogenous nucleic acid according to the invention (e.g. with a length of about 20 to 500 bases or longer), hybridizing, preferably under stringent conditions, determining the hybridizing nucleic acids and, where appropriate, comparing with a standard; or

b) incubating a biological sample with a defined amount of oligonucleotide primer pairs with specificity for a PARP homolog-encoding nucleic acid, amplifying the nucleic acid, determining the amplification product and, where appropriate, comparing with a standard.

The invention further relates to a method for the qualitative or quantitative determination of a PARP homolog according to the invention, which comprises

a) incubating a biological sample with at least one binding partner specific for a PARP homolog,
b) detecting the binding partner/PARP complex and, where appropriate,
c) comparing the result with a standard.

The binding partner in this case is preferably an anti-PARP antibody or a binding fragment thereof, which carries a detectable label where appropriate.

The determination methods according to the invention for PARP, in particular for PARP homologs and for the coding nucleic acid sequences thereof, are suitable and advantageous for diagnosing sepsis- or ischemia-related tissue damage, in particular strokes, myocardial infarcts, diabetes or septic shock.

The invention further comprises a method for determining the efficacy of PARP effectors, which comprises

a) incubating a PARP homolog according to the invention with an analyte which comprises an effector of a physiological or pathological PARP activity; removing the effector again where appropriate; and
b) determining the activity of the PARP homolog, where appropriate after adding substrates or cosubstrates.

The invention further relates to gene therapy compositions which comprise in a vehicle acceptable for gene therapy a nucleic acid construct which

a) comprises an antisense nucleic acid against a coding nucleic acid according to the invention; or

b) a ribozyme against a noncoding nucleic acid according to the invention; or

c) codes for a specific PARP inhibitor.

The invention further relates to pharmaceutical compositions comprising, in a pharmaceutically acceptable vehicle, at least one PARP protein according to the invention, at least one PARP binding partner according to the invention or at least one coding nucleotide sequence according to the invention.

Finally, the invention relates to the use of binding partners of a PARP homolog for the diagnosis or therapy of pathological states in the development and/or progress of which at least one PARP protein, in particular a PARP homolog according to the invention, or a polypeptide derived therefrom, is involved. The binding partner used can be, for example, a low molecular weight binding partner whose molecular weight can be, for example, less than about 2000 dalton or less than about 1000 dalton.

The invention additionally relates to the use of PARP binding partners for the diagnosis or therapy of pathological states mediated by an energy deficit. An energy deficit for the purpose of the present invention is, in particular, a cellular energy deficit which is to be observed in the unwell patient systemically or in individual body regions, organs or organ regions, or tissues or tissue regions. This is characterized by an NAD and/or ATP depletion going beyond (above or below) the physiological range of variation of the NAD and/or ATP level and mediated preferably by a protein with PARP activity, in particular a PARP homolog according to the invention, or a polypeptide derived therefrom.

"Energy deficit-mediated disorders" for the purpose of the invention additionally comprise those in which tissue damage is attributable to cell death resulting from necrosis or apoptosis. The methods according to the invention are suitable for treating and preventing tissue damage resulting from cell damage due to apoptosis or necrosis; damage to nerve tissue due to ischemias and/or reperfusion; neurological disorders; neurodegenerative disorders; vascular stroke; for treating and preventing cardiovascular disorders; for treating other disorders or conditions such as, for example, age-related macular degeneration, AIDS or other immunodeficiency disorders; arthritis; atherosclerosis; cachexia; cancer; degenerative disorders of the skeletal muscles; diabetes; cranial trauma; inflammatory disorders of the gastrointestinal tract such as, for example, Crohn's disease; muscular dystrophy; osteoarthritis; osteoporosis; chronic and/or acute pain; kidney failure; retinal ischemia; septic shock (such as, for example,

endotoxin shock); aging of the skin or aging in general; general manifestations of aging. The methods according to the invention can additionally be employed for extending the life and the proliferative capacity of body cells and for sensitizing tumor cells in connection with irradiation therapy.

The invention particularly relates to the use of a PARP binding partner as defined above for the diagnosis or therapy (acute or prophylactic) of pathological states mediated by energy deficits and selected from neurodegenerative disorders, or tissue damage caused by sepsis or ischemia, in particular of neurotoxic disturbances, strokes, myocardial infarcts, damage during or after infarct lysis (e.g. with TPA, Reteplase or mechanically with laser or Rotablator) and of microinfarcts during and after heart valve replacement, aneurysm resections and heart transplants, trauma to the head and spinal cord, infarcts of the kidney (acute kidney failure, acute renal insufficiency or damage during and after kidney transplant), damages of skeletal muscle, infarcts of the liver (liver failure, damage during or after a liver transplant), peripheral neuropathies, AIDS dementia, septic shock, diabetes, neurodegenerative disorders occuring after ischemia, trauma (craniocerebral trauma), massive bleeding, subarachnoid hemorrhages and stroke, as well as neurodegenerative disorders like Alzheimer's disease, multi-infarct dementia, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis, epilepsy, especially of generalized epileptic seizures such as petit mal and tonoclonic seizures and partial epileptic seizures, such as temporal lobe, and complex partial seizures, kidney failure, also in the chemotherapy of tumors and prevention of metastasis and for the treatment of inflammations and rheumatic disorders, e.g. of rheumatoid arthritis; further for the treatment of revascularization of critically narrowed coronary arteries and critically narrowed peripheral arteries, e.g. leg arteries.

"Ischemia" comprises for the purposes of the invention a localized undersupply of oxygen to a tissue, caused by blockage of arterial blood flow. Global ischemia occurs when the blood flow to the entire brain is interrupted for a limited period. This may be caused, for example, by cardiac arrest. Focal ischemia occurs when part of the brain is cut off from its normal blood supply. Focal ischemia may be caused by thromboembolic closure of a blood vessel, by cerebral trauma, edemas or brain tumor. Even transient ischemias can lead to wideranging neuronal damage. Although damage to "nerve tissue" may occur days or weeks after the start of the ischemia, some permanent damage (e.g. necrotic cell death) occurs in the first few minutes after interruption of the blood supply. This damage is caused, for example, by the neurotoxicity

of glutamate and follows secondary reperfusion, such as, for example, release of free radicals (e.g. oxygen free radicals, NO free radicals). Ischemias may likewise occur in other organs and tissues such as, for example, in the heart (myocardial infarct and other cardiovascular disorders caused by occlusion of the coronary arteries) or in the eye (ischemia of the retina).

The invention additionally relates to the use of an effective therapeutic amount of a PARP binding partner for influencing neuronal activity. "Neuronal activity" for the purposes of the invention may consist of stimulation of damaged neurons, promotion of neuronal regeneration or treatment of neuronal disorders.

"Neuronal damage" for the purposes of the invention comprises every type of damage to "nerve tissue" and every physical or mental impairment or death resulting from this damage. The cause of the damage may be, for example, metabolic, toxic, chemical or thermal in nature and includes by way of example ischemias, hypoxias, trauma, cerebrovascular damage, operations, pressure, hemorrhages, irradiation, vasospasms, neurodegenerative disorders, infections, epilepsy, perception disorders, disturbances of glutamate metabolism and the secondary effects caused thereby.

"Nerve tissue" for the purposes of the invention comprises the various components forming the nervous system, consisting of, inter alia, neurons, glia cells, astrocytes, Schwann cells, the vascular system inside and for supplying, the CNS, brain, brain stem, spinal cord, peripheral nervous system etc.

"Neuroprotective" for the purposes of the invention comprises the reduction, the cessation, the slowing down or the improvement of neuronal damage and the protection, the restoration and the regeneration of nerve tissue which was exposed to neuronal damage.

"Prevention of neurodegenerative disorders" includes the possibility of preventing, slowing down and improving neurodegenerative disorders in people for whom such a disorder has been diagnosed or who are included in appropriate risk groups for these neurodegenerative disorders. Treatments for people already suffering from symptoms of these disorders are likewise meant.

"Treatment" for the purposes of the invention comprises

(i) preventing a disorder, a disturbance or a condition in people with a predisposition thereto;

(ii) preventing a disorder, a disturbance or a condition by slowing down its advance; and

(iii) improving a disorder, a disturbance or a condition.

Examples of "neurological disorders" which can be treated by the methods according to the invention are neuralgias (trigeminal, glossopharyngeal), myasthenia gravis, muscular dystrophies, amyorophic lateral sclerosis (ALS), progressive muscular atrophy, peripheral neuropathies caused by poisoning (e.g. lead poisoning), Guillain-Barré syndrome, Huntington's disease, Alzheimer's disease, Parkinson's disease, or plexus disorders. The methods according to the invention are preferably suitable for treating neurological disorders selected from peripheral neuropathies caused by physical injury or illness; cranial trauma such as, for example, traumatic brain injury; physical damage to the spinal cord; stroke associated with brain damage, such as vascular stroke in conjunction with hypoxia and brain damage, and cerebral reperfusion damage; demyelinating disorders (myelopathies, Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis).

The methods according to the invention can additionally be used for treating cardiovascular disorders. "Cardiovascular disorders" for the purposes of the invention comprise those which cause ischemias or are caused by ischemias or ischemia/reperfusion of the heart. Examples are coronary vessel disorders (for example atherosclerosis), angina pectoris, myocardial infarct, cardiovascular damage due to cardiac arrest or bypass operation.

The methods according to the invention can be used for treating cancer or for sensitizing cancer cells for irradiation therapy. The term "cancer" is to be understood in the widest sense. Modulators of the proteins according to the invention can be used as "anti-cancer therapy agents". For example, the methods can be used for treating types of cancer or tumor cells, such as ACTH-producing tumors, acute lymphatic or lymphoblastic leukemia; acute or chronic lymphocytic leukemia; acute nonlymphocytic leukemia; bladder cancer; brain tumors; breast cancer; cervical carcinoma; chronic myelocytic leukemia; bowel cancer; T-zone lymphoma; endometriosis; esophageal cancer; gall bladder cancer; Ewing's sarcoma; head and neck cancer; cancer of the tongue; Hodgkin's lymphoma; Kaposi's sarcoma; renal cancer; liver cancer; lung cancer; mesothelioma; multiple myeloma; neuroblastoma; non-Hodgkin lymphoma; osteosarcoma; ovarian carcinoma; glioblastoma; mammary carcinoma; cervical carcinoma; prostate cancer; pancreatic cancer; penis cancer; retinoblastoma; skin cancer; stomach

cancer; thyroid cancer; uterine carcinoma; vaginal carcinoma; Wilm's tumor; or trophoblastoma.

"Radiosensitizer" or "irradiation sensitizer" for the purposes of the invention relates to molecules which increase the sensitivity of the cells in the body to irradiation with electromagnetic radiation (for example X-rays) or speed up this irradiation treatment. Irradiation sensitizers increase the sensitivity of cancer cells to the toxic effects of the electromagnetic radiation. Those disclosed in the literature include mitomycin C, 5-bromodeoxyuridine and metronidazole. It is possible to use radiation with wavelengths in the range from 10^{-20} to 10 meters, preferably gamma rays (10^{-20} to 10^{-13} m), X-rays (10^{-11} to 10^{-9} m), ultraviolet radiation (10 nm to 400 nm), visible light (400 nm to 700 nm), infrared radiation (700 nm to 1 mm) and microwave radiation (1 mm to 30 cm).

Disorders which can be treated by such a therapy are, in particular, neoplastic disorders, benign or malignant tumors and cancer. The treatment of other disorders using electromagnetic radiation is likewise possible.

The present invention will now be described in more detail with reference to the appended figures. These show:

In Figure 1 a sequence alignment of human PARP (human PARP1) and two PARPs preferred according to the invention (human PARP2, human PARP3, murine PARP3). Sequence agreements between human PARP1 and human PARP2, human PARP3 or murine PARP3 are depicted within frames. The majority sequence is indicated over the alignment. The zinc finger motifs of human PARP1 are located in the sequence sections corresponding to amino acid residues 21 to 56 and 125 to 162;

In Figure 2 Northern blots with various human tissues to illustrate the tissue distribution of PARP2 and PARP3 molecules according to the invention. Lane 1: brain; lane 2: heart; lane 3: skeletal muscle; lane 4: colon; lane 5: thymus; lane 6: spleen; lane 7: kidney; lane 8: liver; lane 9: intestine; lane 10: placenta; lane 11: lung; lane 12: peripheral blood leukocytes; the respective position of the size standard (kb) is indicated.

In Figure 3 a Northern blot with further various human tissues to illustrate the tissue distribution of the PARP3 molecule according to the invention. Lane 1: heart; lane 2: brain; lane 3: placenta; lane 4: lung; lane 5: liver; lane 6: skeletal muscle; lane

7: kidney; lane 8: pancreas; the respective position of the size standard (kb) is indicated.

In Figure 4 a Western blot with various human tissues to illustrate the tissue distribution of the PARP3 molecule according to the invention at the protein level. Lane 1: heart; lane 2: lung; lane 3: liver; lane 4: spleen; lane 5: kidney; lane 6: colon; lane 7: muscle; lane 8: brain; the respective position of the size standard (kD) is indicated.

In Figure 5 a Western blot with various human tissues to illustrate the tissue distribution of the PARP3 molecule according to the invention. Lane 1: frontal cortex; lane 2: posterior cortex; lane 3: cerebellum; lane 4: hippocampus; lane 5: olfactory bulb; lane 6: striatum; lane 7: thalamus; lane 8: midbrain; lane 9: entorhinal cortex; lane 10: pons; lane 11: medulla; lane 12: spinal cord.

In Figure 6 a diagrammatic representation of the PARP assay (ELISA)

In Figure 7 a diagrammatic representation of the PARP assay (HTRF)

Further preferred embodiments of the invention are described in the following sections.

PARP homologs and functional equivalents

Unless stated otherwise, for the purposes of the present description amino acid sequences are indicated starting with the N terminus. If the one-letter code is used for amino acids, then G is glycine, A is alanine, V is valine, L is leucine, I is isoleucine, S is serine, T is threonine, D is aspartic acid, N is asparagine, E is glutamic acid, Q is glutamine, W is tryptophan, H is histidine, R is arginine, P is proline, K is lysine, Y is tyrosine, F is phenylalanine, C is cysteine and M is methionine.

The present invention is not confined to the PARP homologs specifically described above. On the contrary, those homologs which are functional equivalents thereof are also embraced. Functional equivalents comprise both natural, such as, for example, species-specific or organ-specific, and artificially produced variants of the proteins specifically described herein. Functional equivalents according to the invention differ by addition, substitution, inversion, insertion and/or deletion of one or more amino acid residues of human PARP2 (SEQ ID NO:2),

human PARP3 (SEQ ID NO: 4 and 6) and mouse PARP3 (SEQ ID:8 and 10), there being at least retention of the NAD-binding function of the protein mediated by a functional catalytic C-terminal domain. Likewise, the poly(ADP-ribose)-producing catalytic activity should preferably be retained. Functional equivalents also comprise where appropriate those variants in which the region similar to the leucine zipper is essentially retained.

It is moreover possible, for example, starting from the sequence for human PARP2 or human PARP3 to replace certain amino acids by those with similar physicochemical properties (bulk, basicity, hydrophobicity, etc.). It is possible, for example, for arginine residues to be replaced by lysine residues, valine residues by isoleucine residues or aspartic acid residues by glutamic acid residues. However, it is also possible for one or more amino acids to be exchanged in sequence, added or deleted, or several of these measures can be combined together. The proteins which have been modified in this way from the human PARP2 or human PARP3 sequence have at least 60%, preferably at least 75%, very particularly preferably at least 85%, homology with the starting sequence, calculated using the algorithm of Pearson and Lipman, Proc. Natl. Acad. Sci (USA) 85(8), 1988, 2444-2448.

The following homologies have been determined at the amino acid level and DNA level between human PARP1, 2 and 3 (FastA program, Pearson and Lipman, loc. cit.):

Amino acid homologies:

	Percent identity	Percent identity in PARP signature
PARP1/PARP2	41.97% (517)	86% (50)
PARP1/PARP3	33.81% (565)	53.1% (49)
PARP2/PARP3	35.20% (537)	53.1% (49)

Numbers in parentheses indicate the number of overlapping amino acids.

DNA Homologies:

	Percent identity in the ORF	Percent identity in PARP signature
PARP1/PARP2	60.81% (467)	77.85% (149)
PARP1/PARP3	58.81% (420)	59.02% (61)
PARP2/PARP3	60.22% (269)	86.36% (22)

Numbers in parentheses indicate the number of overlapping nucleotides.

The polypeptides according to the invention can be classified as homologous poly(ADP-ribose) polymerases on the basis of the great similarity in the region of the catalytic domain.

It is also essential to the invention that the novel PARP homologs do not have conventional zinc finger motifs. This means that these enzymes are not necessarily involved in DNA repair or are so in a way which differs from PARP1, but are still able to carry out their pathological mechanism (NAD^+ consumption and thus energy consumption due to ATP consumption). The strong protein expression, particularly of PARP3, observable in the Western blot suggests a significant role in the NAD consumption. This is particularly important for drug development. Potential novel inhibitors of the polymerases according to the invention can thus inhibit the pathological functions without having adverse effects on the desired physiological properties. This was impossible with inhibitors against the PARPs known to date since there was always also inhibition of the DNA repair function. The potentially mutagenic effect of known PARP inhibitors is thus easy to understand. It is also conceivable to design PARP inhibitors so that they efficiently inhibit all PARP homologs with high affinity. In this case, a potentiated effect is conceivable where appropriate.

The PARP homolog which is preferred according to the invention and is shown in SEQ ID NO:2 (human PARP2) can advantageously be isolated from human brain, heart, skeletal muscle, kidney and liver. The expression of human PARP2 in other tissues or organs is distinctly weaker.

The PARP homolog which is preferred according to the invention and is shown in SEQ ID NO: 4 and 6 (human PARP3) can advantageously be isolated from human brain (in this case very preferentially from the hippocampus), heart, skeletal muscle, liver or kidney. The expression of human PARP3 in other tissues or organs, such as muscle or liver, is distinctly weaker.

The skilled worker familiar with protein isolation will make use of the combination of preparative methodologies which is most suitable in each case for isolating natural PARPs according to the invention from tissues or recombinantly prepared PARPs according to the invention from cell cultures. Suitable standard preparative methods are described, for example, in Cooper, T.G., Biochemische Arbeitsmethoden, published by Walter de Gruyter, Berlin, New York or in Scopes, R. Protein Purification, Springer Verlag, New York, Heidelberg, Berlin.

The invention additionally relates to PARP2 and PARP3 homologs which, although they can be isolated from other eukaryotic species, i.e. invertebrates or vertebrates, especially other mammals such as, for example, mice, rats, cats, dogs, pigs, sheep, cattle, horses or monkeys, or from other organs such as, for example the myocardium, have the essential structural and functional properties predetermined by the PARPs according to the invention.

In particular, the human PARP2 which can be isolated from human brain, and its functional equivalents, are preferred agents for developing inhibitors of neurodegenerative diseases as for example stroke. This is because it can be assumed that drug development based on PARP2 as indicator makes it possible to develop inhibitors which are optimized for use in the human brain. However, it cannot be ruled out that inhibitors developed on the basis of PARP2 can also be employed for treating PARP-mediated pathological states in other organs, too (see tissue distribution of the proteins according to the invention).

PARP2 and presumably PARP3 are also, similar to PARP1, activated by damaged DNA, although by a presumably different mechanism. Significance in DNA repair is conceivable. Blockade of the PARPs according to the invention would also be beneficial in indications such as cancer (e.g. in the radiosensitization of tumor patients).

Another essential biological property of PARPs according to the invention and their functional equivalents is to be seen in their ability to bind an interacting partner. Human PARP2 and 3 differ

from previously disclosed PARPs from higher eukaryotes such as, in particular, mammals by having potential so-called leucine zipper motifs. This is a typical motif for protein-protein interactions. It is possible that these motifs permit modulation of PARP activity by an interacting partner. This additional structural element thus also provides a possible starting point for development of PARP effectors such as, for example, inhibitors.

The invention thus further relates to proteins which interact with PARP2 and/or 3, preferably those which bring about their activation or inactivation.

The invention further relates to proteins which still have the abovementioned ligand-binding activity and which can be prepared starting from the specifically disclosed amino acid sequences by targeted modifications.

It is possible, starting from the peptide sequence of the proteins according to the invention, to generate synthetic peptides which are employed, singly or in combination, as antigens for producing polyclonal or monoclonal antibodies. It is also possible to employ the PARP protein or fragments thereof for generating antibodies. The invention thus also relates to peptide fragments of PARP proteins according to the invention which comprise characteristic partial sequences, in particular those oligo- or polypeptides which comprise at least one of the abovementioned sequence motifs. Fragments of this type can be obtained, for example, by proteolytic digestion of PARP proteins or by chemical synthesis of peptides.

Novel specific PARP2 and PARP3 binding partners

Active and preferably selective inhibitors against the proteins according to the invention were developed using the specific assay systems described above for binding partners for PARP2 and PARP3. These inhibitors optionally are also active vis a vis PARP1.

Inhibitors provided according to the invention have a strong inhibitory activity on PARP2. The K_i values may in this case be less than about 1000 nM, such as less than about 700 nM, less than about 200 nM or less than about 30 nM, e.g. about 1 to 20 nM.

Inhibitors according to the invention may also have a surprising selectivity for PARP2. This is shown by the K_i(PARP1) : K_i(PARP2) ratio for such inhibitors according to the invention which is,

for example, greater than 3 or greater than 5, as for example greater than 10 or greater than 20.

An example which should be mentioned is 4-(N-(4-hydroxyphenyl)aminomethyl)-(2H)-dihydrophthalazine-1-one. The preparation of this and other analogous compounds may be performed according to Puodzhyunas et al., Pharm. Chem. J. 1973, 7, 566 or Mazkanowa et al., Zh. Obshch. Khim., 1958, 28, 2798, or Mohamed et al., Ind. J. Chem. B., 1994, 33, 769 each incorporated by reference.

The above identified compuound shows a Ki value of 113 nM for PARP2 and is eight times more selective for PARP2 than for PARP3.

Nucleic acids coding for PARP homologs:

Unless stated otherwise, nucleotide sequences are indicated in the present description from the 5′ to the 3′ direction.

The invention further relates to nucleic acid sequences which code for the abovementioned proteins, in particular for those having the amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8 and 10, but without being restricted thereto. Nucleic acid sequences which can be used according to the invention also comprise allelic variants which, as described above for the amino acid sequences, are obtainable by deletion, inversion, insertion, addition and/or substitution of nucleotides, preferably of nucleotides shown in SEQ ID NO: 1, 3, 7 and 9, but with essential retention of the biological properties and the biological activity of the corresponding gene product. Nucleotide sequences which can be used are obtained, for example, by nucleotide substitutions causing silent (without alteration of the amino acid sequence) or conservative amino acid changes (exchange of amino acids of the same size, charge, polarity or solubility).

Nucleic acid sequences according to the invention also embrace functional equivalents of the genes, such as eukaryotic homologs for example from invertebrates such as Caenorhabditis or Drosophila, or vertebrates, preferably from the mammals described above. Preferred genes are those from vertebrates which code for a gene product which has the properties essential to the invention as described above.

The nucleic acids according to the invention can be obtained in a conventional way by various routes:

For example, a genomic or a cDNA library can be screened for DNA which codes for a PARP molecule or a part thereof. For example, a cDNA library obtained from human brain, heart or kidney can be screened with a suitable probe such as, for example, a labeled single-stranded DNA fragment which corresponds to a partial sequence of suitable length selected from SEQ ID NO: 1 or 3, or sequence complementary thereto. For this purpose, it is possible, for example, for the DNA fragments of the library which have been transferred into a suitable cloning vector to be, after transformation into a bacterium, plated out on agar plates. The clones can then be transferred to nitrocellulose filters and, after denaturation of the DNA, hybridized with the labeled probe. Positive clones are then isolated and characterized.

The DNA coding for PARP homologs according to the invention or partial fragments can also be synthesized chemically starting from the sequence information contained in the present application. For example, it is possible for this purpose for oligonucleotides with a length of about 100 bases to be synthesized and sequentially ligated in a manner known per se by, for example, providing suitable terminal restriction cleavage sites.

The nucleotide sequences according to the invention can also be prepared with the aid of the polymerase chain reaction (PCR). For this, a target DNA such as, for example, DNA from a suitable full-length clone is hybridized with a pair of synthetic oligonucleotide primers which have a length of about 15 bases and which bind to opposite ends of the target DNA. The sequence section lying between them is then filled in with DNA polymerase. Repetition of this cycle many times allows the target DNA to be amplified (cf. White et al.(1989), Trends Genet. 5, 185).

The nucleic acid sequences according to the invention are also to be understood to include truncated sequences, single-stranded DNA or RNA of the coding and noncoding, complementary DNA sequence, mRNA sequences and cDNAs derived therefrom.

The invention further embraces nucleotide sequences hybridizing with the above sequences under stringent conditions. Stringent hybridization conditions for the purpose of the present invention exist when the hybridizing sequences have a homology of about 70 to 100%, such as, for example about 80 to 100% or 90 to 100% (preferably in an amino acid section of at least about 40, such as, for example, about 50, 100, 150, 200, 400 or 500 amino acids).

Stringent conditions for the screening of DNA, in particular cDNA banks, exist, for example, when the hybridization mixture is washed with 0.1X SSC buffer (20X SSC buffer = 3M NaCl, 0.3M sodium citrate, pH 7.0) and 0.1% SDS at a temperature of about 60°C.

Northern blot analyses are analyses are washed under stringent conditions with 0.1X SSC, 0,1% SDS at a temperature of about 65°C, for example.

Nucleic acid derivatives and expression constructs:

The nucleic acid sequences are also to be understood to include derivatives such as, for example, promoter variants or alternative splicing variants. The promoters operatively linked upstream of the nucleotide sequences according to the invention may moreover be modified by nucleotide addition(s) or substitution(s), inversion(s), insertion(s) and/or deletion(s), but without impairing the functionality or activity of the promoters. The promoters can also have their activity increased by modifying their sequence, or be completely replaced by more effective promoters even from heterologous organisms. The promoter variants described above are used to prepare expression cassettes according to the invention.

Specific examples of human PARP2 splicing variants which may be mentioned are:

Variant human PARP2a: Deletion of base pairs 766 to 904 (cf. SEQ ID NO:1). This leads to a frame shift with a new stop codon ("TAA" corresponding to nucleotides 922 to 924 in SEQ ID NO:1).
Variant human PARP2b: Insertion of
5'- gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg -3'
after nucleotide 204 (SEQ ID NO:1). This extends the amino acid sequence by the insertion: GMPGRSWASKRVS

Nucleic acid derivatives also mean variants whose nucleotide sequences in the region from -1 to -1000 in front of the start codon have been modified so that gene expression and/or protein expression is increased.

Besides the nucleotide sequence described above, the nucleic acid constructs which can be used according to the invention comprise in functional, operative linkage one or more other regulatory sequences, such as promoters, amplification signals, enhancers, polyadenylation sequences, origins of replication, reporter genes, selectable marker genes and the like. This linkage may,

depending on the desired use, lead to an increase or decrease in gene expression.

In addition to the novel regulatory sequences, it is possible for the natural regulatory sequence still to be present in front of the actual structural genes. This natural regulation can, where appropriate, be switched off by genetic modification, and the expression of the genes increased or decreased. However, the gene construct may also have a simpler structure, that is to say no additional regulatory signals are inserted in front of the structural genes, and the natural promoter with its regulation is not deleted. Instead, the natural regulatory sequence is mutated in such a way that regulation no longer takes place, and gene expression is enhanced or diminished. It is also possible to insert additional advantageous regulatory elements at the 3′ end of the nucleic acid sequences. The nucleic acid sequences can be present in one or more copies in the gene construct.

Advantageous regulatory sequences for the expression method according to the invention are, for example, present in promoters such as cos, tac, trp, tet, trp-tet, lpp, lac, lpp-lac, lacIq, T7, T5, T3, gal, trc, ara, SP6, l-PR or the l-PL promoter, which are advantageously used in Gram-negative bacteria. Other advantageous regulatory sequences are present, for example, in the Gram-positive promoters amy and SPO2, in the yeast promoters ADC1, MFa, AC, P-60, CYC1, GAPDH or in the plant promoters CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or in the ubiquitin or phaseolin promoter.

It is possible in principle to use all natural promoters with their regulatory sequences. It is also possible and advantageous to use synthetic promoters.

Said regulatory sequences are intended to make specific expression of the nucleic acid sequences and protein expression possible. This may mean, for example, depending on the host organism that the gene is expressed or overexpressed only after induction, or that it is immediately expressed and/or overexpressed.

The regulatory sequences or factors may moreover preferably have a positive influence on, and thus increase or decrease, the expression. Thus, enhancement of the regulatory elements may advantageously take place at the level of transcription by using strong transcription signals such as promoters and/or enhancers.

However, it is also possible to enhance translation by, for example, improving the stability of the mRNA.

Enhancers mean, for example, DNA sequences which bring about increased expression via an improved interaction between RNA polymerase and DNA.

The recombinant nucleic acid construct or gene construct is, for expression in a suitable host organism, advantageously inserted into a host-specific vector which makes optimal expression of the genes in the host possible. Vectors are well known to the skilled worker and are to be found, for example, in "Cloning Vectors" (Pouwels P. H. et al., Ed., Elsevier, Amsterdam-New York-Oxford, 1985). Apart from plasmids, vectors also mean all other vectors known to the skilled worker, such as, for example, phages, viruses, such as SV40, CMV, baculovirus and adenovirus, transposons, IS elements, phasmids, cosmids, and linear or circular DNA. These vectors may undergo autonomous replication in the host organism or chromosomal replication.

Expression of the constructs:

The recombinant constructs according to the invention described above are advantageously introduced into a suitable host system and are expressed. Cloning and transfection methods familiar to the skilled worker are preferably used in order to bring about expression of said nucleic acids in the particular expression system. Suitable systems are described, for example, in Current Protocols in Molecular Biology, F. Ausubel et al., ed., Wiley Interscience, New York 1997.

Suitable host organisms are in principle all organisms which make it possible to express the nucleic acids according to the invention, their allelic variants, their functional equivalents or derivatives or the recombinant nucleic acid construct. Host organisms mean, for example, bacteria, fungi, yeasts, plant or animal cells. Preferred organisms are bacteria such as those of the genera Escherichia, such as, for example, Escherichia coli, Streptomyces, Bacillus or Pseudomonas, eukaryotic microorganisms such as Saccharomyces cerevisiae, Aspergillus, higher eukaryotic cells from animals or plants, for example Sf9 or CHO cells.

The gene product can also, if required, be expressed in transgenic organisms such as transgenic animals such as, in particular, mice, sheep, or transgenic plants. The transgenic organisms may also be so-called knock-out animals or plants in which the corresponding endogenous gene has been switched off,

such as, for example, by mutation or partial or complete deletion.

The combination of the host organisms and the vectors appropriate for the organisms, such as plasmids, viruses or phages, such as, for example, plasmids with the RNA polymerase/promoter system, phages λ, μ or other temperate phages or transposons and/or other advantageous regulatory sequences forms an expression system. The term expression systems preferably means, for example, a combination of mammalian cells such as CHO cells, and vectors, such as pcDNA3neo vector, which are suitable for mammalian cells.

As described above, the gene product can also be expressed advantageously in transgenic animals, e.g. mice, sheep, or transgenic plants. It is likewise possible to program cell-free translation systems with the RNA derived from the nucleic acid.

The gene product can also be expressed in the form of therapeutically or diagnostically suitable fragments. To isolate the recombinant protein it is possible and advantageous to use vector systems or oligonucleotides which extend the cDNA by certain nucleotide sequences and thus code for modified polypeptides which serve to simplify purification. Suitable modifications of this type are, for example, so-called tags which act as anchors, such as, for example, the modification known as the hexa-histidine anchor, or epitopes which can be recognized as antigens by antibodies (described, for example, in Harlow, E. and Lane, D., 1988, Antibodies: A Laboratory Manual. Cold Spring Harbor (N.Y.) Press). These anchors can be used to attach the proteins to a solid support such as, for example, a polymer matrix, which can, for example, be packed into a chromatography column, or to a microtiter plate or to another support.

These anchors can also at the same time be used to recognize the proteins. It is also possible to use for recognition of the proteins conventional markers such as fluorescent dyes, enzyme markers which form a detectable reaction product after reaction with a substrate, or radioactive markers, alone or in combination with the anchors for derivatizing the proteins.

Production of antibodies:

Anti-PARP2 antibodies are produced in a manner familiar to the skilled worker. Antibodies mean both polyclonal, monoclonal, human or humanized antibodies or fragments thereof, single chain antibodies or also synthetic antibodies, likewise antibody fragments such as Fv, Fab and $F(ab')_2$. Suitable production methods

are described, for example, in Campbell, A.M., Monoclonal Antibody Technology, (1987) Elsevier Verlag, Amsterdam, New York, Oxford and in Breitling, F. and Dübel, S., Rekombinante Antikörper (1997), Spektrum Akademischer Verlag, Heidelberg.

Further use of the coding sequence:

The present cDNA additionally provides the basis for cloning the genomic sequence of the novel PARP genes. This also includes the relevant regulatory or promoter sequence, which is available, for example, by sequencing the region located 5′ upstream of the cDNA according to the invention or located in the introns of the genes. The cDNA sequence information is also the basis for producing antisense molecules or ribozymes with the aid of known methods (cf. Jones, J.T. and Sallenger, B.A. (1997) Nat. Biotechnol. 15, 902; Nellen, W. and Lichtenstein, C. (1993) TIBS, 18, 419). The genomic DNA can likewise be used to produce the gene constructs described above.

Another possibility of using the nucleotide sequence or parts thereof is to generate transgenic animals. Transgenic overexpression or genetic knock-out of the sequence information in suitable animal models may provide further valuable information about the (patho)physiology of the novel genes.

Therapeutic applications:

In situations where there is a prevailing deficiency of a protein according to the invention it is possible to employ several methods for replacement. On the one hand, the protein, natural or recombinant, can be administered directly or by gene therapy in the form of its coding nucleic acid (DNA or RNA). It is possible to use any suitable vectors for this, for example both viral and non-viral vehicles. Suitable methods are described, for example, by Strauss and Barranger in Concepts in Gene Therapy (1997), Walter de Gruyter, publisher. Another alternative is provided by stimulation of the endogenous gene by suitable agents.

It is also possible to block the turnover or the inactivation of PARPs according to the invention, for example by proteases. Finally, inhibitors or agonists of PARPs according to the invention can be employed.

In situations where a PARP is present in excess or is overactivated, various types of inhibitors can be employed. This inhibition can be achieved both by antisense molecules,

ribozymes, oligonucleotides or antibodies, and by low molecular weight compounds.

The active substances according to the invention, i.e. PARP proteins, nucleic acids and PARP binding partners such as, for example, antibodies or modulators, can be administered either as single therapeutic active substances or as mixtures with other therapeutic active substances. They can be administered as such, but in general they are administered in the form of pharmaceutical compositions, i.e. as mixtures of the active substance(s) with at least one suitable pharmaceutical carrier or diluent. The active substances or compositions can be administered in any way suitable for the particular therapeutic purpose, e.g. orally or parenterally.

The nature of the pharmaceutical composition and of the pharmaceutical carrier or diluent depends on the required mode of administration. Oral compositions can be, for example, in the form of tablets or capsules and may contain customary excipients such as binders (e.g. sirup, acacia, gelatin, sorbitol, tragacanth or polyvinylpyrrolidone), bulking agents (e.g. lactose, sugar, corn starch, calcium phosphate, sorbitol or glycine), lubricants (e.g. magnesium stearate, talc, polyethylene glycol or silica), disintegrants (e.g. starch) or wetting agents (e.g. sodium lauryl sulfate). Oral liquid products may be in the form of aqueous or oily suspensions, solutions, emulsions, sirups, elixirs or sprays etc. or may be in the form of dry powders for reconstitution with water or another suitable carrier. Liquid products of these types may contain conventional additives, for example suspending agents, flavorings, diluents or emulsifiers. It is possible to employ for parenteral administration solutions or suspensions with conventional pharmaceutical carriers. Parenteral administration of active substances according to the invention advantageously takes place using a liquid pharmaceutical composition which can be administered parenterally, in particular intravenously. This preferably contains an effective amount of at least one active substance, preferably in dissolved form, in a pharmaceutically acceptable carrier suitable for this purpose. Examples of pharmaceutical carriers suitable for this purpose are, in particular, aqueous solutions such as, for example, physiological saline, phosphate-buffered saline, Ringer's solution, Ringer's lactate solution and the like. The composition may moreover contain further additions such as antioxidants, chelating agents or antimicrobial agents.

The choice in each case of the dosage of the active substances according to the invention and the particular dosage schedule are subject to a decision of the treating physician. The latter will select a suitable dose and an appropriate dosage schedule depending on the chosen route of administration, on the efficacy of the medicine in each case, on the nature and severity of the disorder to be treated, and on the condition of the patient and his response to the therapy. Thus, for example, the pharmacologically active substances can be administered to a mammal (human or animal) in doses of about 0.5 mg to about 100 mg per kg of body weight and day. They can be administered in a single dose or in several doses.

Nontherapeutic applications:

The nucleic acids according to the invention, such as, for example, cDNA, the genomic DNA, the promoter, and the polypeptide, and partial fragments thereof, can also be used in recombinant or nonrecombinant form for developing various test systems.

For example, it is possible to establish a test system which is suitable for measuring the activity of the promoter or of the protein in the presence of a test substance. The methods of measurement in this case are preferably simple ones, e.g. colorimetric, luminometric, fluorimetric, immunological or radioactive, and allow preferably a large number of test substances to be measured rapidly. Tests of this type are suitable and advantageous for so-called high-throughput screening. These test systems allow test substances to be assessed for their binding to or their agonism, antagonism or inhibition of proteins according to the invention.

Determination of the amount, activity and distribution of the proteins according to the invention or their underlying mRNA in the human body can be used for the diagnosis, for the determination of the predisposition and for the monitoring of certain diseases. Likewise, the sequence of the cDNA and the genomic sequence may provide information about genetic causes of and predispositions to certain diseases. It is possible to use for this purpose both DNA/RNA probes and antibodies of a wide variety of types. The nucleotide sequences according to the invention or parts thereof can further be used in the form of suitable probes for detecting point mutations, deletions or insertions.

The proteins according to the invention can further be used to identify and isolate their natural ligands or interacting partners. The proteins according to the invention can additionally be used to identify and isolate artificial or synthetic ligands. For this purpose, the recombinantly prepared or purified natural protein can be derivatized in such a way that it has modifications which permit linkage to support materials. Proteins bound in this way can be incubated with various analytes, such as, for example, protein extracts or peptide libraries or other sources of ligands. Specifically bound peptides, proteins or low molecular weight, non-proteinogenous substances can be isolated and characterized in this way. Non-proteinogenous substances mean, for example, low molecular weight chemical substances which may originate, for example, from classical drug synthesis or from so-called substance libraries which have been synthesized combinatorially.

The protein extracts used are derived, for example, from homogenates of plants or parts of plants, microorganisms, human or animal tissues or organs.

Ligands or interacting partners can also be identified by methods like the yeast two-hybrid system (Fields, S. and Song, O. (1989) Nature, 340, 245). The expression banks which can be employed in this case may be derived, for example, from human tissues such as, for example, brain, heart, kidney etc.

The nucleic acid sequences according to the invention and the proteins encoded by them can be employed for developing reagents, agonists and antagonists or inhibitors for the diagnosis and therapy of chronic and acute diseases associated with the expression or activation of one of the protein sequences according to the invention, such as, for example, with increased or decreased expression thereof. The reagents, agonists, antagonists or inhibitors developed can subsequently be used to produce pharmaceutical preparations for the treatment or diagnosis of disorders. Examples of possible diseases in this connection are those of the brain, of the peripheral nervous system, of the cardiovascular system or of the eye, of septic shock, of rheumatoid arthritis, diabetes, acute kidney failure, or of cancer.

The relevance of the proteins according to the invention for said indications was verified using specific inhibitors in relevant animal models.

The invention is now illustrated in detail with reference to the following examples.

Example 1: Isolation of the PARP2 and PARP3 cDNA

The present cDNA sequences were found for the first time on sequence analysis of cDNA clones of a cDNA library from human brain (Human Brain 5'Stretch Plus cDNA Library, # HL3002a, Clontech). The mouse PARP3 clones were isolated from a "lambda triplex mouse brain cDNA library" (Clontech order No. ML5004t). The sequences of these clones are described in SEQ ID NO:1, 3, 7 and 9.

Example 2: Expression of PARP2 and PARP3 in human tissues

The expression of human PARP2 and human PARP3 was investigated in twelve different human tissues by Northern blot analysis. A Human Multiple Tissue Northern Blot (MTN™) supplied by Clontech (#7760-1 and #7780-1) was hybridized for this purpose with an RNA probe. The probe was produced by in vitro transcription of the corresponding cDNA of human PARP2 and human PARP3 in the presence of digoxigenin-labeled nucleotides in accordance with the manufacturer's method (BOEHRINGER MANNHEIM DIG Easy Hyb order No. 1603 558, DIG Easy Hyb method for RNA:RNA hybridization). The protocol was modified to carry out the prehybridization: 2x1h with addition of herring sperm DNA (10 mg/ml of hybridization solution). Hybridization then took place overnight with addition of herring sperm DNA (10 mg/ml of hybridization solution). The bands were detected using the CDP-Star protocol (BOEHRINGER MANNHEIM CDP-Star™ order No. 1685 627).

After stringent washing, the transcript of PARP2 was mainly detected in human brain, heart, skeletal muscle, kidney and liver. The transcript size of about 1.9 kb corresponds to the length of the cDNA determined (1.85kb) (cf. Figure 2(A)).

In other tissues or organs, human PARP2 expression is considerably weaker.

After stringent washing, the transcript of PARP3 was mainly detected in heart, brain, kidney, skeletal muscle and liver. Expression in other tissues (placenta, lung, pancreas) is distinctly weaker (cf. Figure 2(B)). There are at least 2 transcripts for human PARP3, which can presumably be explained by different polyadenylation sites or alternative splicing. Their size (about 2.2 kb and 2.5 kb respectively) corresponds to the length of the cDNA determined (2.3kb). Washing was carried out

with 0.2 x SSC/0.2% SDS at room temperature for 2 x 15 minutes and then with 0.1 x SSC/0.1% SDS at 65°C for 2 x 15 minutes (prepared from 20X SSC: 3M NaCl, 0.3M sodium citrate, pH 7.0).

Example 3: Production of antibodies

Specific antibodies against the proteins according to the invention were produced. These were used inter alia for analyzing the tissue distribution at the protein level of PARP2 and PARP3 by immunoblot (Western blot) analysis. Examples of the production of such antibodies are indicated below.

The following peptides were prepared by synthesis in the manner familiar to the skilled worker for the antibody production. In some cases, a cysteine residue was attached to the N or C terminals of the sequences in order to facilitate coupling to KLH (keyhole limpet hemocyanin).

PARP-2: NH_2-MAARRRRSTGGGRARALNES-CO_2H (amino acids 1-20; SEQ ID NO: 23)
NH_2-KTELQSPEHPLDQHYRNLHC-CO_2H (amino acids 335-353; SEQ ID NO: 24)

PARP-3: NH_2-CKGRQAGREEDPFRSTAEALK-CO_2H (amino acids 25-44 SEQ ID NO: 25)
NH_2-CKQQIARGFEALEALEEALK-CO_2H (amino acids 230-248; SEQ ID NO: 26)

The production of an anti-PARP3 antibody is described as a representative example.

For human PARP3, polyclonal antibodies were raised in rabbits using a synthetic peptide having the peptide sequence H_2N-KQQIARGFEALEALEEALK-CO_2H (SEQ ID NO: 27)(amino acids 230-248 of the human PARP3 protein sequence). The corresponding mouse sequence differs in this region only by one amino acid (H_2N-KQQIARGFEALEALEEAMK-CO_2H; SEQ ID NO: 28). A cysteine was also attached to the N terminus in order to make it possible for the protein to couple to KLH.

Rabbits were immunized a total of five times, at intervals of 7-14 days, with the KLH-peptide conjugate. The antiserum obtained was affinity-purified using the antigen. The specific IgG fraction was isolated from the serum using the respective peptides which, for this purpose, were initially immobilized on an affinity column in the manner familiar to the skilled worker. The respective antiserum was loaded onto this affinity column, and non-specifically sorbed proteins were eluted with buffer. The spe-

cifically bound IgG fraction was eluted with 0.2 M glycine/HCl buffer pH 2.2. The pH was immediately increased using a 1M TRIS/HCl buffer pH 7.5. The eluate containing the IgG fraction was mixed 1:1 (volume) with saturated ammonium sulfate solution and incubated at +4°C for 30 min to complete the precipitation. The resulting precipitate was centrifuged at 10,000 g and, after removal of the supernatant, dissolved in the minimum amount of PBS/TBS. The resulting solution was then dialyzed against PBS/TBS in the ratio 1:100 (volume). The antibodies were adjusted to a concentration of about 100 µg of IgG/ml. The PARP3 antibodies purified in this way had high specificity for PARP3. Whereas mouse PARP3 was recognized well, there was no observable cross-reaction with PARP1 or PARP2.

Example 4: Analysis of the tissue distribution by immunoblot (Western blot)

The tissue distribution at the protein level was also investigated for PARP2 and PARP3 by immunoblot (Western blot) analysis.

Preparation of the mouse tissues for protein gels:

Tissues or cells were homogenized using a Potter or Ultra-Turrax. For this, 0.5 g of tissue (or cells) was incubated in 5 ml of buffer (10 mM Tris-HCl pH 7.5, 1 mM EDTA, 6 mM $MgCl_2$), one tablet of protease inhibitor cocktail (Boehringer Mannheim, order No.: 1836153) and benzonase (purity grade I, MERCK) at 37°C for 30 min. Tissue samples from mice were produced for heart, lung, liver, spleen, kidney, intestine, muscle, brain and for human embryonic kidney cells (HEK293, human embryonal kidney).

Protein gels:

The NuPAGE system supplied by NOVEX was used according to the instructions for protein gels. Polyacrylamide gels (NuPAGE 4-12% BisTris, NOVEX NP 0321), running buffer (MES-Running Buffer, NOVEX NP 0002), antioxidant (NOVEX NP 0005), protein size standard (Multi Mark Multi Colored Standard, NOVEX LC 5725), sample buffer (NuPAGE LDS Sample Buffer (4X), NOVEX NP 0007) were used. The gels were run for 45 minutes at a voltage of 200 V.

Western blot:

Western blots were carried out using the NOVEX system in accordance with instructions. A nitrocellulose membrane (Nitrocellulose Pore size 45 µm, NOVEX LC 2001) was used. The transfer took 1 hour at a current of 200 mA. The transfer buffer consisted of 50 ml of

transfer buffer concentrate (NOVEX NP 0006), 1 ml of antioxidant (NOVEX NP 0002), 100 ml of analytical grade methanol and 849 ml of double-distilled water.

Besides the blots produced in this way, also used were premade blots, for example from Chemicon (mouse brain blot, Chemicon, catalog No.: NS 106 with the tissues 1. frontal cortex, 2. posterior cortex, 3. cerebellum, 4. hippocampus, 5. olfactory bulb, 6. striatum, 7. thalamus, 8. mid brain, 9. entorhinal cortex, 10. pons, 11. medulla, 12. spinal cord).

Antibody reaction with PARP3:

The Western blots were blocked in TBST (TBS + 0.3 % Tween 20) with 5% dry milk powder for at least 2 hours (TBS: 100 mM Tris pH 7.5, 200 mM NaCl). The antibody reaction with the primary antibody (dilution 1:1000) took place in TBST with 5% dry milk powder (see above) at room temperature for at least 2 hours or at 4°C overnight, with gentle agitation (vertical rotator). This was followed by washing three times in TBST for 5 minutes. Incubation with the secondary antibody (anti-rabbit IgG, peroxidase-coupled, SIGMA A-6154, dilution 1:2000) took place in TBST with 5% dry milk powder for 1 hour. This was followed by washing three times for 5 minutes each time as above. The subsequent detection was based on chemiluminescence using the SUPER BLAZE kit (Pierce, Signal BLAZE Chemiluminescent Substrate 34095) as stated by the manufacturer. The "Lumi-Film" (Chemiluminescent Detection Film, Boehringer order No: 1666916) was used. The films were developed for about 2 min (X-ray developer concentrate, ADEFO-Chemie GmbH), hydrated, fixed for about 4 min (Acidofix 85 g/l /AGFA), hydrated and then dried.

Example 5: Preparation of the enzymes

For comparison, human PARP1 was expressed recombinantly in the baculovirus system in the manner familiar to the skilled worker and partially purified as described (Shah et al., Analytical Biochemistry 1995, 227, 1-13). Bovine PARP1 in a purity of 30-50% (c= 0.22 mg/ml, spec. activity 170 nmol of ADP-ribose/min/mg of total protein at 25°C) was purchased from BIOMOL (order No. SE-165). Human and mouse PARP2 and PARP3 were expressed recombinantly in the baculovirus system (Bac-to-Bac system, BRL LifeScience). For this purpose, the appropriate cDNAs were cloned to the pFASTBAC-1 vector. Preparation of recombinant baculovirus DNA by recombination in E. coli was followed by transfection of insect cells (Sf9 or High-Five) with the appropriate recombinant baculovirus DNAs. Expression of the corresponding proteins was veri-

fied by Western blot analysis. Virus strains were amplified in the manner familiar to the skilled worker. Larger amounts of recombinant proteins were obtained by infecting 500 ml of insect cell culture (2 x 10^6 cells/ml) with viruses in an MOI (multiplicity of infection; ratio of viruses to cells) of 5-10 and incubating for 3 to 4 days. The insect cells were then pelleted by centrifugation, and the proteins were purified from the pellet.

The purification took place by classical methods of protein purification familiar to the skilled worker, detecting the enzymes with appropriate specific antibodies. In some cases, the proteins were also affinity-purified on a 3-aminobenzamide affinity column as described (Burtscher et al., Anal Biochem 1986, 152:285-290). The purity was >90%.

Example 6: Assay systems for determining the activity of PARP2 and PARP3 and the inhibitory action of effectors on PARP1, PARP2 and PARP3.

a) Production of antibodies against poly(ADP-ribose)

It is possible to use poly(ADP-ribose) as antigen for generating anti-poly(ADP-ribose) antibodies. The production of anti-poly(ADP-ribose) antibodies is described in the literature (Kanai Y et al. (1974) Biochem Biophys Res Comm 59:1, 300-306; Kawamaitsu H et al. (1984) Biochemistry 23, 3771-3777; Kanai Y et al. (1978) Immunology 34, 501-508).

The following were used, inter alia: anti-poly(ADP-ribose) antibodies (polyclonal antiserum, rabbits), BIOMOL; order No. SA-276, anti-poly(ADP-ribose) antibodies (monoclonal, mouse; clone 10H; hybridoma supernatant, affinity-purified).

The antisera or monoclonal antibodies obtained from hybridoma supernatant were purified by protein A affinity chromatography in the manner familiar to the skilled worker.

b) ELISA

Materials:

ELISA color reagent: TMB mix, SIGMA T-8540

A 96-well microtiter plate (FALCON Micro-Test III™ Flexible Assay Plate, # 3912) was coated with histones (SIGMA, H-7755). Histones were for this purpose dissolved in carbonate buffer (0.05M Na_2HCO_3; pH 9.4) in a concentration of 50 µg/ml. The individual

wells of the microtiter plate were each incubated with 150 µl of this histone solution at room temperature for at least 2 hours or at 4°C overnight. The wells are then blocked by adding 150 µl of a 1% BSA solution (SIGMA, A-7888) in carbonate buffer at room temperature for 2 hours. This is followed by three washing steps with washing buffer (0.05% Tween10 in 1x PBS; PBS (Phosphate buffered saline; Gibco, order No. 10010): 0.21g/l KH_2PO_4, 9g/l NaCl, 0.726g/l $Na_2HPO_4 \cdot 7H_2O$, pH 7.4). Washing steps were all carried out in a microtiter plate washer ("Columbus" microtiter plate washer, SLT-Labinstruments, Austria).

Required for the enzyme reaction were an enzyme reaction solution and a substrate solution, in each case as a premix. The absolute amount of these solutions depended on the intended number of assay wells.

Composition of the enzyme reaction solution per well:
- 4 µl of PARP reaction buffer (1M Tris-HCl pH 8.0, 100mM $MgCl_2$, 10mM DTT)
- 20ng of PARP1 (human or bovine) or 8ng PARP2 (human or mouse)
- 4 µl of activated DNA (1 mg/ml; SIGMA, D-4522)
- H_2O ad 40 µl

Composition of the substrate solution per well:
- 5 µl of PARP reaction buffer (10x)
- 0.8 µl of NAD solution (10mM, SIGMA N-1511)
- 44 µl H_2O

Inhibitors were dissolved in 1x PARP reaction buffer. DMSO, which was occasionally used to dissolve inhibitors in higher concentrations, was no problem up to a final concentration of 2%. For the enzyme reaction, 40 µl of the enzyme reaction solution were introduced into each well and incubated with 10 µl of inhibitor solution for 10 minutes. The enzyme reaction was then started by adding 50 µl of substrate solution per well. The reaction was carried out at room temperature for 30 minutes and then stopped by washing three times with washing buffer.

The primary antibodies employed were specific anti-poly(ADP-ribose) antibodies in a dilution of 1:5000. Dilution took place in antibody buffer (1% BSA in PBS; 0.05% Tween20). The incubation time for the primary antibodies was one hour at room temperature. After subsequently washing three times with washing buffer, incubation was carried out with the secondary antibody (anti-mouse IgG, Fab fragments, peroxidase-coupled, Boehringer Mannheim, order No. 1500.686; anti-rabbit IgG, peroxidase-coupled, SIGMA, order No. A-6154) in a dilution of 1:10,000 in antibody buffer at

room temperature for one hour. Washing three times with washing buffer was followed by the color reaction using 100 µl of color reagent (TMB mix, SIGMA) per well at room temperature for about 15 min. The color reaction was stopped by adding 100 µl of 2M H_2SO_4. This was followed by immediate measurement in an ELISA plate reader (EAR340AT "Easy Reader", SLT-Labinstruments, Austria) (450nm versus 620nm). The measurement principle is depicted diagrammatically in Figure 6.

Various concentrations were used to construct a dose-effect plot to determine the K_i value of an inhibitor. Values are obtained in triplicate for a particular inhibitor concentration. Arithmetic means are determined using Microsoft© Excel. The IC_{50} is determined using the Microcal© Origin Software (Vers. 5.0) ("Sigmoidal Fit"). Conversion of the IC_{50} value is calculated in this way into K_i values took place by using "calibration inhibitors". The "calibration inhibitors" were also measured in each analysis. The K_i values of the "calibration inhibitors" were determined in the same assay system by analysis of the Dixon diagram in the manner familiar to the skilled worker.

b) HTRF (homogenous time-resolved fluorescence) assay

In the HTRF PARP assay according to the invention, histones, as target proteins for modification by PARP, are labeled indirectly with an XL665 fluorophore. The anti poly(ADP ribose) antibody is directly labeled with a europium cryptate (anti-PAR-cryptate). If the XL665 fluorophore is in the direct vicinity in space, which is ensured by binding to the poly(ADP-ribose) on the histone, then energy transfer is possible. The emission at 665 nm is thus directly proportional to the amount of bound antibody, which in turn is equivalent to the amount of poly(ADP-ribose). The measured signal thus corresponds to the PARP activity. The measurement principle is depicted diagrammatically in Figure 7. The materials used are identical to those used in the ELISA (see above) unless expressly indicated.

Histones were dissolved in a concentration of 3 mg/ml in Hepes buffer (50mM, pH=7.5). Biotinylation took place with sulfo-NHS-LC-biotin (Pierce, #21335T). A molar ratio of 4 biotin molecules per histone was used. The incubation time was 90 minutes (RT). The biotinylated histones were then purified on a G25 SF HR10/10 column (Pharmacia, 17-0591-01) in Hepes buffer (50mM, pH=7.0) in order to remove excess biotinylation reagent. The anti-poly(ADP-ribose) antibody was labeled with europium cryptate using bifunctional coupling reagents (Lopez, E. et al., Clin. Chem. 39(2), 196-201 (1993); US Patent 5,534,622).

Purification took place on a G25SF HR10/30 column. A molar ratio of 3.1 cryptates per antibody was achieved. The yield was 25%. The conjugates were stored at -80°C in the presence of 0.1% BSA in phosphate buffer (0.1M, pH=7).

For the enzyme reaction, the following were pipetted into each well:
- 10 µl of PARP solution in PARP HTRF reaction buffer (50mM Tris-HCl pH 8.0, 10mM $MgCl_2$, 1mM DTT) with 20ng of PARP1 (human or bovine) or 8ng of PARP2 (human or mouse)
- 10 µl of activated DNA in PARP HTRF reaction buffer (50µg/ml)
- 10 µl of biotinylated histones in PARP HTRF reaction buffer (1.25µM)
- 10 µl of inhibitor in PARP HTRF reaction buffer

These reagents were incubated for 2 minutes before the reaction was started by adding
- 10 µl of NAD solution in PARP HTRF reaction buffer (41 µM/ml). The reaction time was 30 minutes at room temperature.

The reaction was then stopped by adding
- 10 µl of PARP inhibitor (25 µM, K_i=10nM) in "Revelation" buffer (100mM Tris-HCl pH 7.2, 0.2M KF, 0.05% BSA).

The following were then added:
- 10 µl of EDTA solution (SIGMA, E-7889, 0.5M in H_2O)
- 100 µl of Sa-XL665 (Packard Instruments) in "Revelation" buffer (15-31.25nM)
- 50 µl of anti-PAR cryptate in "Revelation" buffer (1.6-3.3nM).

Measurement was then possible after 30 minutes (up to 4 hours). The measurement took place in a "discovery HTRF microplate analyzer" (Canberra Packard Instruments). The K_i values were calculated as described for the ELISA.

Example 7: Test systems for determining the therapeutic efficacy of PARP inhibitors

Novel PARP inhibitors can have their therapeutic efficacy checked in relevant pharmacological models. Examples of some suitable models are listed in Table 1.

Disorder	Model	Literature
Neurodegenerative disorders (stroke, Parkinson's, etc.)	NMDA excitotoxicity in mice or rats	See below for description
Stroke	Permanent MCAO ("middle cerebral arterial occlusion")	Tokime, T. et al., J. Cereb. Blood Flow Metab., 18(9): 991-7, 1998. Guegan, C., Brain Research. Molecular Brain Research, 55(1): 133-40, 1998.
	Transient, focal MCAO in rats or mice	Eliasson MJL et al., Nat Med 1997, 3:1089-1095. Endres, M et al., J Cereb Blood Flow Metab 1997, 17:1143-1151. Takahashi K et al., J Cereb Blood Flow Metab 1997, 17:1137-1142.
Parkinson's disease	MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine) toxicity in mice/rats	Cosi C, et al. , Brain Res. , 1998 809(1):58-67. Cosi C, et al. , Brain Res., 1996 729(2):264-9.
Myocardial infarct	Coronary vessel occlusion in rats, pigs or rabbits	Richard V, et al., Br. J. Pharmacol 1994, 113, 869-876. Thiemermann C, et al., Proc Natl Acad Sci U S A. 1997, 94(2):679-83. Zingarelli B, et al. , Cardiovasc Res. 1997, 36(2):205-15.
	Langendorf heart model in rats or rabbits	See below for description
Septic shock	Endotoxin shock in rats	Szabo C, et al., J Clin Invest, 1997, 100(3):723-35.

	Zymosan- or carrageenan-induced multiple organ failure in rats or mice	Szabo C, et al. J Exp Med. 1997, 186(7):1041-9.Cuzzocrea S, et al. Eur J Pharmacol. 1998, 342(1):67-76.
Rheumatoid arthritis	Adjuvant- or collagen-induced arthritis in rats or mice	Szabo C, et al., Proc Natl Acad Sci U S A. 1998, 95(7):3867-72.
Diabetes	Streptozotocin- and alloxan-induced or obesity-associated	Uchgata Y et al., Diabetes 1983, 32: 316-318.Masiello P et al., Diabetologia 1985, 28: 683-686.Shimabukuro M et al., J Clin Invest 1997, 100: 290-295.
Cancer	In vitro model; see below	Schlicker et al., 1999, 75(1), 91-100.

a) NMDA excitotoxicity model

Glutamate is the most important excitory neurotransmitter in the brain. Under normal conditions, glutamate is secreted into the synaptic cleft and stimulates the post-synaptic glutamate receptors, specifically the glutamate receptors of the "NMDA" and "AMPA" types. This stimulation plays a significant part in numerous functions of the brain, including learning, memory and motor control.

Under the conditions of acute and chronic neurodegeneration (e.g. stroke), however, there is a great increase in the presynaptic glutamate secretion, resulting in excessive stimulation of the receptors. This leads to death of the cells stimulated in this way. These increased glutamate activities occur in a number of neurological disorders or psychological disturbances and lead to states of overexcitation or toxic effects in the central nervous system (CNS) but also in the peripheral nervous system. Thus, glutamate is involved in a large number of neurodegenerative disorders, in particular neurotoxic disturbances following hypoxia, anoxia, ischemia and after lesions like those occurring after stroke and trauma, and stroke, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis (ALS; "Lou Gehring's disease"), cranial trauma, spinal cord trauma, peripheral neuropathies, AIDS dementia and Parkinson's disease. Another disease in which glutamate receptors are important is epilepsy (cf. Brain

Res Bull 1998; 46(4):281-309, Eur Neuropsychopharmacol 1998, 8(2):141-52.).

Glutamate effects are mediated through various receptors. One of these receptors is called the NMDA (N-methyl-D-aspartate) receptor after a specific agonist (Arzneim.Forschung 1990, 40, 511-514; TIPS, 1990, 11, 334-338; Drugs of the Future 1989, 14, 1059-1071). N-Methyl-D-aspartate is a strong agonist of a particular class of glutamate receptors ("NMDA" type). Stimulation of the NMDA receptor leads to influx of calcium into the cell and the generation of free radicals. The free radicals lead to DNA damage and activation of PARP. PARP in turn causes cell death through depletion of high-energy phosphates (NAD and ATP) in the cell. This explains the toxicity of NMDA. Treatment of animals with NMDA can therefore be regarded as a model of the abovementioned disorders in which excitotoxicity is involved.

Because of the importance of glutamate receptors in neurodegeneration, many pharmacological approaches to date have been directed at specific blocking of precisely these receptors. However, because of their importance in normal stimulus conduction, these approaches have proved to be problematic (side effects). In addition, stimulation of the receptors is an event which takes place very rapidly so that administration of the receptors often comes too late ("time window" problem). Thus there is a great need for novel principles of action and inhibitors of NMDA-related neurotoxicity.

Protection against cerebral overexcitation by excitatory amino acids (NMDA antagonism in mice) can be regarded as adequate proof of the activity of a pharmacological effector of PARP in disorders based on excitotoxicity. Intracerebral administration of excitatory amino acids (EAA) induces such massive overexcitation that it leads within a short time to convulsions and death of the animals (mice).

In the present case there was unilateral intracerebroventricular administration of 10 µl of a 0.035% strength aqueous NMDA solution 120 minutes after intraperitoneal (i.p.) administration of the test substance. These symptoms can be inhibited by systemic, e.g. intraperitoneal, administration of centrally acting drugs. Since excessive activation of EAA receptors in the central nervous system plays an important part in the pathogenesis of various neurological disorders, information can be gained from the detected EAA antagonism in vivo about possible therapeutic utilizability of the substances for such CNS disorders. An ED50 at which 50% of the animals are, due to preceding i.p.

administration of the measured substance, free of symptoms with a fixed dose of NMDA was determined as a measure of the activity of the substances.

b) Langendorf heart model (model for myocardial infarct)

Male Sprague-Dawley rats (bodyweight 300-400 g; origin Janvier, Le Genest-St-Isle, France) were used for the test. The rats were treated orally by gavage with the active substance or placebo (volume: 5 ml/kg). 50 minutes later, heparin is administered intraperitoneally (Liquemin N Roche, 125 IU/animal in 0.5 ml). The animals are anesthesized with Inactin® T133 (thiobetabarbital sodium 10%), fixed on the operating table, tracheotomized and ventilated with a "Harvard ventilatory pump" (40 beats/min, 4.5 ml/beat). Thoracotomy was followed by immediate catheterization of the aorta, removal of the heart and immediate retrograde perfusion. The hearts were perfused with a constant pressure of 75 mmHg, which is achieved using a "Gilson Miniplus 2 perfusion pump". Composition of the perfusate (mmol/l): NaCl 118, KCl 4.7, $CaCl_2$ x 2 H_2O 2.52, $MgSO_4$ x 7 H_2O 1.64, $NaHCO_3$ 24.88, KH_2PO_4 1.18, glucose 11. The temperature is kept at 37°C throughout the experiment. Functional parameters were continuously recorded using a "Gould 4-channel recorder". Measurements were made of the left-ventricular pressure (LVP; mmHg), LVEDP (mmHg), enzyme release (creatine kinase, mU/ml/g), coronary flow rate (ml/min), HR (pulse rate, min^{-1}). The left-ventricular pressure was measured using a liquid-filled latex balloon and a Statham23 Db pressure transducer. The volume of the balloon was initially adjusted to reach an LVEDP (left-ventricular end-diastolic pressure) of about 12 mmHg. The dP/dt_{max} (maximum pumping force) is derived from the pressure signal using a differentiator module. The heart rate was calculated from the pressure signal. The flow rate was determined using a drop counter (BMT Messtechnik GmbH Berlin). After an equilibration time of 20 minutes, the hearts were subjected to a 30-minute global ischemia by stopping the perfusate supply while keeping the temperature at 37°C. During the following 60-minute reperfusion period, samples of the perfusate were taken after 3, 5, 10, 15, 30, 45 and 60 min for analysis of creatine kinase (CK) activity. Means and standard deviations for the measured parameters were analyzed statistically (Dunnett test). The significance limit was p=0.05.

The experiment on rabbit hearts was carried out similarly. Male white New Zealand rabbits (obtained from: Interfauna) were used. The hearts were prepared as described above for the rat model. The perfusion pressure was set at a maximum of 60 mmHg and the flow rate at about 25ml/min. The equilibration time was about

30 min. The substance was administered by infusion directly upstream of the heart. 15 min after starting the infusion, a 30-minute global ischemia was caused by stopping the flow while maintaining the temperature of the heart. A 30-minute reperfusion followed. Perfusate was taken for investigation of CK activity before administration of the substance, after 15 min and at various times (5, 10, 15, 20, 30 min) during the reperfusion. The following parameters were measured: LVP (mmHg), LVEDP, LVdP/dt, PP (mmHg), HR (pulse rate; beats/min), CK activity (U/min/g heart weight).

c) Animal model for acute kidney failure

The protective effect of intravenous administration of PARP inhibitors (4 days) on the kidney function of rats with postischemic acute kidney failure was investigated.

Male Sprague-Dawley rats (about 330 g at the start of the experiments; breeder: Charles River) were used. 10-15 animals were employed per experimental group. Administration of active substance/placebo took place continuously with an osmotic micropump into the femoral vein. Orbital blood was taken (1.5 ml of whole blood) under inhalation anesthesia with enflurane (Ethrane Abbot, Wiesbaden).

After the initial measurements (blood sample) and determination of the amount of urine excreted in 24h, the rats were anesthetized ("Nembutal", pentobarbital sodium, Sanofi CEVA; 50mg/kg i.p., volume injected 1.0 ml/kg) and fastened on a heatable operating table (37°C). 125 IU/kg heparin (Liquemin N, Roche) were administered i.v. into the caudal vein. The abdominal cavity was opened and the right kidney was exposed. The branching-off renal artery was exposed and clamped off superiorly using bulldog clamps (Diefenbach 38mm). The left renal artery was likewise exposed and clamped off (superiorly, about half way to the kidney). During the operation, an osmotic micropump was implanted into the femoral vein. The intestine was reinserted and the fluid loss was compensated with luke-warm 0.9% NaCl. The animals were covered with a moist cloth and kept warm under red light. After 40 min, the appearance of the kidneys was recorded, and the clamps were removed, first the right then the left. The intestine was put back and 2 drops of antibiotic (Tardomyocel, Bayer) were added. The abdominal wall was closed with sterile cat gut (Ethicon No.4) and treated once more with 1 drop of antibiotic. The epidermis was sutured with sterile Ethibond Exel (Ethicon) No.3/0, and the

suture was sprayed with Nebacetin N (Yamanouchi) wound spray. A tenth of a daily dose of drug/placebo is given as i.v. bolus.

Samples and blood were taken for investigating biochemical parameters in the serum and urine: Na, K, creatinine, protein (only in urine), on days 1, 2 and 4 of the experiment. In addition, the feed and water consumption, bodyweight and urine volume were recorded. After 14 days, the animals were sacrificed and the kidneys were assessed.

The assessment excluded all animals which died of an infarct during the experiment or showed an infarct at necropsy on day 14. The creatinine clearance and the fractional sodium excretion were calculated as kidney function parameters, comparing treated animals with control and sham.

d) In vitro model for radiosensitization (tumor therapy)

MCF-7-cells (human breast carcinoma) were cultivated in Dulbecco's modified Eagle's medium with 10% heat-inactivated FCS and 2 mM L-glutamine. Cells were seeded out overnight in cell densities of 100, 1000 or 10,000 cells per well in a 6-well plate and then exposed to ionizing radiation with a dose in the range from 0 to 10 Gy (^{137}Cs, Shepard Mark, model I-68A, dose rate 3.28 Gy/min). 10 days after the irradiation, the experiment was assessed, counting colonies with fifty cells as positive.

e) Stroke model (focal cerebral ischemia; MCA (middle cerebral artery) occlusion on a rat)

A focal ischemia was performed by means of cauterisation of the right distal MCA on Sprague-Dawley or Long-Evans rats. The rats may be treated before or after the beginning of the MCA occlusion with modulators of the proteins of the invention. As a rule, doses of 1-10 mg/kg are chosen (bolus application), optionally followed by a continuous infusion of 0.5-5 mg/kg/h.

The rats are anesthetised with halothane in a mixture of 70 % nitrogen and 30 % oxygen (4% at initial phase and 0.8-1.2 % during the operation). The body temperature was permanently measured rectally and was kept constant at 37.5 °C ± 0.5 °C by means of a controllable heating blanket. Moreover, arterial blood pressure, arterial pH, ($Pa(O_2)$ and $Pa(CO_2)$ were optionally measured by means of a tail vein catheder. Thereafter, the focal iscehmia was carried out using the method of Chen et al. (Stroke 17: 738-743; 1986) or Liu et al. (Am. J. Physiol. 256: H589-593; 1989) by means of continuous cauterisation of the distal part of the right

MCA. When the operation was terminated, the animals were kept in a warm environment for a further 24 hours. Then they were killed with the use of CO_2 and decapitated. Their brains were taken, shock-frozen (dry ice or liquid nitrogen) and stored at -80 °C. The brains were cut into 0.02 mm thick slices and every 20th cut was used for the subsequent analysis. The corresponding cuts are stained with cresyl violet (Nissl staining). Alternatively, TTC (2,3,4-triphenyltetrazoliumchloride) may be used for staining. The infarct volume may then be analysed under a microscope. For exact quantification, a computer-based image analyzing software may be used (J. Cereb. Clood Flow Metabol. 10: 290-293; 1990).

f) Septic shock

Groups of 10 male C57/BL mice (body weight 18-20 g) are treated with LPS (lipopolysaccharide, from E. coli, LD_{100} 20 mg/animal i. v.) plus galactosamine (20 mg/animal i. v.). the substance to be tested is applied i. p. or i. v. during three succeeding days (e. g. 1-10 mg/kg), with the first dose being administered 30 minutes after the LPS treatment. The death rate is determined every 12 hours. Alternatively, the substance may also be applied in several doses spread over the days.

g) Determination of altered gene expression in aging cells

The aging of cells is simulated by changing the cell culture media from the complete medium with a reduced serum concentration and thereafter is analysed by means of quantitative PCR or Northern Blotting (Linskens et al., Nucleic Acids Res. 1995, 23(16): 3244-51). As typical markers for the aging of the skin for example collagen or elastin may be used. Human fibroblasts or fibroblast cell lines are used which simulate the aging of the skin. Modulators of the proteins of the invention are added to the medium and their effect on the changing of the gene expression is observed. An increased production of elastin in cells with a reduced aging process caused by means of said modulators may be observed.